

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

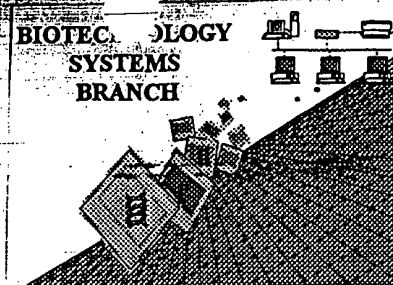
For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

E Kemmerer

RAW SEQUENCE LISTING **ERROR REPORT**



#9
EOK 12/13/00

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/265,585

Source: 1646

Date Processed by STIC: 11-24-00

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

1646

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/265,585

DATE: 11/24/2000
TIME: 12:30:35

Input Set : A:\5914-066 sequence listing.txt
Output Set: N:\CRF3\11242000\I265585.raw

3 <110> APPLICANT: Benfey et al.
5 <120> TITLE OF INVENTION: Scarecrow Gene, Promoter and Uses Thereof
7 <130> FILE REFERENCE: 5914-066-999
9 <140> CURRENT APPLICATION NUMBER: 09/265,585
10 <141> CURRENT FILING DATE: 1999-03-10
12 <150> PRIOR APPLICATION NUMBER: 08/842,445
13 <151> PRIOR FILING DATE: 1997-04-24
15 <150> PRIOR APPLICATION NUMBER: 08/638,617
16 <151> PRIOR FILING DATE: 1996-04-26
18 <160> NUMBER OF SEQ ID NOS: 144
20 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply
Corrected Diskette Needed
See pp. 1, 2, 3

ERRORED SEQUENCES

5584 <210> SEQ ID NO: 116
5585 <211> LENGTH: 380
5586 <212> TYPE: PRT
5587 <213> ORGANISM: Arabidopsis thaliana
5589 <400> SEQUENCE: 116
5591 Thr Ser Val Cys Ser Arg Glu Thr Val Met Glu Ile Ala Thr Ala Ile
5592 1 5 10 15
5593 Ala Glu Gly Lys Thr Glu Ile Ala Thr Glu Ile Leu Ala Arg Val Ser
5594 20 25 30
5595 Gln Thr Pro Asn Leu Glu Arg Asn Ser Glu Glu Lys Leu Val Asp Phe
5596 35 40 45
5597 Met Val Ala Ala Leu Arg Ser Arg Ile Ala Ser Pro Val Thr Glu Leu
5598 50 55 60
5599 Tyr Gly Lys Glu His Leu Ile Ser Thr Gln Leu Tyr Glu Leu Ser
5600 65 70 75 80
5601 Pro Cys Phe Lys Leu Gly Phe Glu Ala Ala Asn Leu Ala Ile Leu Asp
5602 85 90 95
5603 Ala Ala Asp Asn Asn Asp Gly Gly Met Met Ile Pro His Val Ile Asp
5604 100 105 110
5605 Phe Asp Ile Gly Glu Gly Gly Gln Tyr Val Asn Leu Leu Arg Thr Leu
5606 115 120 125
5607 Ser Thr Arg Arg Asn Gly Lys Ser Gln Ser Gln Asn Ser Pro Val Val
5608 130 135 140
5609 Lys Ile Thr Ala Val Ala Asn Asn Val Tyr Gly Cys Leu Val Asp Asp
5610 145 150 155 160
5611 Gly Gly Glu Glu Arg Leu Lys Ala Val Gly Asp Leu Leu Ser Gln Leu
5612 165 170 175
E--> 5613 ly Asp Arg Leu Gly Ile Ser Val Ser Phe Asn Val Val Thr Ser Leu
5614 180 185 190
E--> 5615 rg Leu Gly Asp Leu Asn Arg Glu Ser Leu Gly Cys Asp Pro Asp Glu
5616 195 200 205
5617 Thr Leu Ala Val Asn Leu Ala Phe Lys Leu Tyr Arg Val Pro Asp Glu

Invalid amino acid designators.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/265,585

DATE: 11/24/2000

TIME: 12:30:36

Input Set : A:\5914-066 sequence listing.txt

Output Set: N:\CRF3\11242000\I265585.raw

```

5618      210      215      220
5619 Ser Val Cys Thr Glu Asn Pro Arg Asp Glu Leu Leu Arg Arg Val Lys
5620 225      230      235      240
5621 Gly Leu Lys Pro Arg Val Val Thr Leu Val Glu Gln Glu Met Asn Ser
5622      245      250      255
5623 Asn Thr Ala Pro Phe Leu Gly Arg Val Ser Glu Ser Cys Ala Cys Tyr
5624      260      265      270
5625 Gly Ala Leu Leu Glu Ser Val Glu Ser Thr Val Pro Ser Thr Asn Ser
5626      275      280      285
5627 Asp Arg Ala Lys Val Glu Glu Gly Ile Gly Arg Lys Leu Val Asn Ala
5628      290      295      300
5629 Val Ala Cys Glu Gly Ile Asp Arg Ile Glu Arg Cys Glu Val Phe Gly
5630 305      310      315      320
5631 Lys Trp Arg Met Arg Met Ser Met Ala Gly Phe Glu Leu Met Pro Leu
5632      325      330      335
5633 Ser Glu Lys Ile Ala Glu Ser Met Lys Ser Arg Gly Asn Arg Val His
5634      340      345      350
5635 Pro Gly Phe Thr Val Lys Glu Asp Asn Gly Gly Val Cys Phe Gly Trp
5636      355      360      365
5637 Met Gly Arg Ala Leu Thr Val Ala Ser Ala Trp Arg
5638      370      375      380

```

← F.Y.I.

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

09/265, 585

p. 3

<210> 16
<211> 26
<212> PRT
<213> Oryza sativa

<221> SITE
<222> 7
<223> Xaa=unknown amino acid

<400> 16

Ile His Val Ile Asp Phe Xaa Leu Gly Val Gly Gly Gln Trp Ala Ser
1 5 10 15

Phe Leu Gln Glu Leu Ala His Arg Arg Gly
20 25

<210> 17
<211> 36
<212> PRT
<213> Zea mays

<221> SITE
<222> 1...36
<223> Xaa=unknown amino acid

<400> 17

Val His Ile Ile Xaa Phe Xaa Leu Met Gln Gly Leu Gln Trp Pro Ala
1 5 10 15

Leu Met Asp Val Phe Ser Ala Arg Lys Gly Gly Pro Pro Lys Leu Arg
20 25 30

Ile Thr Gly Ile
35

<210> 18
<211> 1085
<212> DNA
<213> Arabidopsis thaliana

<221> modified_base
<222> 1...1085
<223> n=a, c, g, or t

<400> 18

→ Missing <220> blank line feature

→ Missing <220> blank line feature

→ Missing <220> blank line feature

* Although a "blank line" feature, <220> heading is mandatory when you have <221>, <222> or <223> features. This error occurs throughout the sequence listing. Please insert <220> feature where needed.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/265,585

DATE: 11/24/2000

TIME: 12:30:37

Input Set : A:\5914-066 sequence listing.txt

Output Set: N:\CRF3\11242000\I265585.raw

L:442 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:442 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:460 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:460 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:513 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:513 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:1173 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:31
L:1173 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:31
L:1254 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:32
L:1254 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:1329 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:33
L:1329 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
L:1392 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:34
L:1392 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
L:1572 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:39
L:1572 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
L:1596 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:40
L:1596 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
L:1599 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:40
M:340 Repeated in SeqNo=40
L:1634 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:42
L:1634 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:42
L:1637 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:42
M:340 Repeated in SeqNo=42
L:1640 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:42
L:1652 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:42
L:1677 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:43
L:1677 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:43
L:1683 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:43
M:340 Repeated in SeqNo=43
L:1692 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:43
L:1846 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:46
L:1846 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:46
L:1920 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:48
L:1920 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:48
L:2005 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:50
L:2005 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:50
L:2071 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:52
L:2071 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:52
L:2184 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:54
L:2184 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:54
L:2371 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:56
L:2371 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:56
L:2442 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:57
L:2442 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:57
L:2444 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:57
M:340 Repeated in SeqNo=57
L:2472 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:57

VERIFICATION SUMMARY DATE: 11/24/2000
PATENT APPLICATION: US/09/265,585 TIME: 12:30:37

Input Set : A:\5914-066 sequence listing.txt
Output Set: N:\CRF3\11242000\I265585.raw

L:2570 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:58
L:2570 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:58
L:2591 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:58
M:340 Repeated in SeqNo=58
L:2594 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:58
L:2636 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:58
L:2660 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:59
L:2660 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:59
L:2682 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:60
L:2682 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:60
L:2684 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:60
M:340 Repeated in SeqNo=60
L:2686 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:60
L:2703 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:61
L:2703 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:61
L:2706 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:61
M:340 Repeated in SeqNo=61
L:2709 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:61
L:2732 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:62
L:2732 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:62
L:2758 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:63
L:2758 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:63
L:2790 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:64
L:2790 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:64
L:2792 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:64
M:340 Repeated in SeqNo=64
L:2812 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:65
L:2812 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:65
L:2815 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:65
M:340 Repeated in SeqNo=65
L:2916 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:67
L:2916 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:67
L:2919 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:67
M:340 Repeated in SeqNo=67
L:2922 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:67
L:2925 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:67
L:2928 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:67
L:2931 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:67
L:2937 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:67
L:3073 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:68
M:340 Repeated in SeqNo=68
L:3100 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:69
L:3126 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:70
L:3155 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:71
L:3177 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:72
L:3204 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:73
L:3240 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:75
M:340 Repeated in SeqNo=75
L:3274 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:76

VERIFICATION SUMMARY DATE: 11/24/2000
PATENT APPLICATION: US/09/265,585 TIME: 12:30:37

Input Set : A:\5914-066 sequence listing.txt
Output Set: N:\CRF3\11242000\I265585.raw

M:340 Repeated in SeqNo=76
L:3310 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:78
L:3337 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:79
L:5613 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:5613 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:5615 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:5615 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:6365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:133
L:6396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135
L:6411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:136
L:6431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137
L:6462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139
L:6481 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140
L:6500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141
L:6531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:143